1. (Four times amended) A method of determining whether a member of a pool of cloned test transcription factor polynucleotides encodes a plant pathway transcription factor, the method comprising: collecting a pool of cloned test transcription factor polynucleotides; introducing into a plant cell a nucleic acid comprising a plant promoter of a pathway gene operably linked to a reporter gene; introducing into the plant cell a member of the pool of cloned test transcription factor polynucleotides, wherein said member is selected on the basis of structural similarity to a known transcription factor for a pathway gene; and detecting expression of said reporter gene in the plant cell, thereby determining whether the member of the cloned test transcription factor polynucleotide pool encodes a plant pathway transcription factor.

3. (Amended) [The method of claim 1,] A method of determining whether one or more members of a pool of cloned test transcription factor polynucleotides encode a plant pathway transcription factor, the method comprising: collecting a pool of cloned test transcription factor polynucleotides; introducing into a plant cell a nucleic acid comprising a plant promoter of a pathway gene operably linked to a reporter gene; introducing into the plant cell said one or more members of the pool of cloned test transcription factor polynucleotides, wherein [a] said members of the cloned test transcription factor polynucleotide pool [is] are selected without regard to structural similarity to a known transcription factor for a pathway gene; and detecting expression of said reporter gene in the plant cell, thereby determining whether one or more members of the cloned test transcription factor polynucleotide pool encode a plant pathway transcription factor.

4. (Amended) The method of claim [1] 3, further comprising detecting the expression of at least one other pathway gene in the cell.

5. (Amended) The method of claim [1] 3, wherein said pathway gene is a biosynthetic pathway gene.

6. (Reiterated) The method of claim 5, wherein said biosynthetic pathway gene is a primary metabolite pathway gene.

7. (Reiterated) The method of claim 5, wherein said biosynthetic pathway gene is a secondary metabolite pathway gene.

8. (Reiterated) The method of claim 7, wherein said secondary metabolite pathway gene is a terpenoid pathway gene.

9. (Reiterated) The method of claim 7, wherein said secondary metabolite pathway gene is an alkaloid pathway gene.

Q3 10. (Amended) The method of claim [1]3, wherein said cloned test transcription factor polynucleotide is from a plant.

11. (Thrice amended) The method of claim [1]3, wherein said cloned test transcription factor polynucleotide is expressed transiently in the plant cell.

Q4 13. (Twice amended) The method of claim [1]3, wherein said plant promoter operably linked to a reporter gene is transiently transfected into the plant cell.

14. (Amended) The method of claim [1]3, wherein said reporter gene is beta-glucuronidase (GUS).

15. (Amended) The method of claim [1]3, wherein said promoter is the promoter of a biosynthetic pathway gene of a plant that produces secondary metabolites.

16. (Reiterated) The method of claim 8, wherein said terpenoid pathway gene is from a species selected from the group consisting of *Mentha* and *Taxus*.

17. (Reiterated) The method of claim 8, wherein said terpenoid pathway gene is selected from the group consisting of limonene synthase and taxadiene synthase.

Q5 18. (Amended) The method of claim [1]3, further comprising deconvoluting the pool of cloned test transcription factor polynucleotides when said pool comprises more than one transcription factor polynucleotide, to identify the minimum number of cloned test transcription factor polynucleotides necessary to detect expression from said pathway gene promoter.

Q6 26. (Amended) A method of determining whether a member of a pool of test transcription factor polynucleotides encodes a biosynthetic pathway transcription factor, comprising introducing into a plant cell nucleic acids comprising the test transcription factor polynucleotides and detecting expression of a biosynthetic pathway gene in the plant cell by quantitation of the biosynthetic pathway gene RNA level,

wherein said member of the pool of test transcription factor polynucleotides is selected without regard to structural similarity to a known transcription factor for a pathway gene.

33. (Four times amended) A method of determining whether two or more members of a pool of cloned test transcription factor polynucleotides are required for expression from a pathway gene promoter, the method comprising: collecting a pool of cloned test transcription factor polynucleotides; introducing into a plant cell a nucleic acid comprising a biosynthetic pathway gene promoter operably linked to a reporter gene; introducing into the plant cell the pool of cloned test transcription factor polynucleotides; and detecting expression from said biosynthetic pathway gene promoter in the plant cell, and deconvoluting the pool of cloned test transcription factor polynucleotides to identify the minimum number of cloned test transcription factor polynucleotides necessary to detect expression from said pathway gene promoter, thereby determining whether two or more members of the cloned test transcription factor polynucleotide pool are required for expression from said biosynthetic pathway gene promoter.

35. (Reiterated) The method of claim 33, wherein a member of the cloned test transcription factor polynucleotide pool is selected on the basis of structural similarity to a known transcription factor for a pathway gene.

36. (Reiterated) The method of claim 33, wherein a member of the cloned test transcription factor polynucleotide pool is selected without regard to structural similarity to a known transcription factor for a pathway gene.

37. (Reiterated) The method of claim 33, further comprising detecting the expression of at least one other pathway gene in the cell.

38. (Amended) The method of claim 33, wherein said pathway gene promoter is operably linked to a biosynthetic pathway gene.

39. (Amended) The method of claim [38] 33, wherein said biosynthetic pathway gene promoter is a primary metabolite pathway gene promoter.

40. (Amended) The method of claim [38] 33, wherein said biosynthetic pathway gene promoter is a secondary metabolite pathway gene promoter.

41. (Amended) The method of claim 40, wherein said secondary metabolite pathway gene promoter is a terpenoid pathway gene promoter.

42. (Amended) The method of claim 40, wherein said secondary metabolite pathway gene promoter is an alkaloid pathway gene promoter.

43. (Reiterated) The method of claim 33, wherein said cloned test transcription factor polynucleotide is from a plant.

44. (Reiterated) The method of claim 33, wherein said cloned test transcription factor polynucleotide is expressed transiently in the cell.

45. (Reiterated) The method of claim 33, wherein said cell is from a plant.

46. (Reiterated) The method of claim 33, wherein said promoter operably linked to a reporter gene is transiently transfected into a cell.

47. (Reiterated) The method of claim 46, wherein said reporter gene is beta-glucuronidase (GUS).

48. (Reiterated) The method of claim 33, wherein said promoter is the promoter of a biosynthetic pathway gene of a plant that produces secondary metabolites.

49. (Reiterated) The method of claim 41, wherein said terpenoid pathway gene is from a species selected from the group consisting of *Mentha* and *Taxus*.

50. (Reiterated) The method of claim 41, wherein said terpenoid pathway gene is selected from the group consisting of limonene synthase and taxadiene synthase.

REMARKS

Amendments to the claims have been made in response the Examiner's comments. No new matter enters the claims or specification by any of these amendments, and Applicants believe that these amendments do not raise new issues.